

QY 421 BETHSCTCPNDQVCTAFLECTVGDASACLTCPAPDNTRCGTCTGNTGYMLSGGLCKEVAE 480
 DB 421 EETHSCTCPNDQVCTAFLECTVGDASACLTCPAPDNTRCGTCTGNTGYMLSGGLCKEVAE 480
 QY 481 STDHYIGFETDLODLEKYLLOKTDRIEVAHFISNDMLNSWFDPSWKRMLLTLSN 540
 DB 481 STDHYIGFETDLODLEKYLLOKTDRIEVAHFISNDMLNSWFDPSWKRMLLTLSN 540
 QY 541 KYKSSLVHMLTGLSLQCLTKNSTLEPLVAVYVNPFGGSHSFWMPVNSPPDWERTK 600
 DB 541 KYKSSLVHMLTGLSLQCLTKNSTLEPLVAVYVNPFGGSHSFWMPVNSPPDWERTK 600
 QY 601 LDLPLOCYNWTILGNKWKTFETVHIYLSRSKNSGPNESIIYEPLEFIDPSRLGY 660
 DB 601 LDLPLOCYNWTILGNKWKTFETVHIYLSRSKNSGPNESIIYEPLEFIDPSRLGY 660
 QY 661 MKINNIQVFGYSMHFDPEARDLILQDYPYTOGSQDSALLQLLEIRDRVNLKSPPGQRR 720
 DB 661 MKINNIQVFGYSMHFDPEARDLILQDYPYTOGSQDSALLQLLEIRDRVNLKSPPGQRR 720
 QY 721 LDLPSCLLHRLKLTSEVVRISQALQAFNAKLPTMTDYDTTKLCS 766
 DB 721 LDLPSCLLHRLKLTSEVVRISQALQAFNAKLPTMTDYDTTKLCS 766

RESULT 2
 Q8KOR9 PRELIMINARY; PRT; 766 AA.
 ID Q8KOR9
 AC Q8KOR9
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE RIKEN cDNA B830045N13.
 GN Name=B830045N13Rik;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Drapletton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek J., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX Strausberg R.;
 RA Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC030498; AAH30498.1; -;
 DR MGD; MGI:2443035; B830045N13Rik.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001862; MAC_perforin.
 DR Pfam; PF01823; MACPF; 1.

DR SMART; SM00181; EGF; 1.
 DR SMART; SM00457; MACPF; 1.
 SQ SEQUENCE 766 AA; 88482 MW; 15BC4F2DAF813B71 CRC64;
 Query Match 98.2%; Score 4009; DB 2; Length 766;
 Best Local Similarity 97.8%; Pred. No. 3.4e-280;
 Matches 749; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MWRSRAGAEFLSMALWEMIALLSHCWVLAVAASDQHATSPFDWLLSDKGFHRSQEY 60
 DB 1 MIWRRRAGAELSSLMALWEMIALLSHCWVLAVAASDQHATSPFDWLLSDKGFHRSQEY 60
 QY 61 TDFVRSRSGFSTRYKIYREFGRKVNLAVERRFLGSPPLAPAEFFNRILRGRRPTL 120
 DB 61 TDFVRSRSGFSTRYKIYREFGRKVNLAVERRFLGSPPLAPAEFFNRILRGRRPTL 120
 QY 121 QOITENLIKKYTHFLLSATLGGESLTI FVDRKRLSKRAEGSDSTNSSSVLTLETHQL 180
 DB 121 QOITENLIKKYTHFLLSATLGGESLTI FVDRKRLSKRAEGSDSTNSSSVLTLETHQL 180
 QY 181 AASYFIDRSTLRLLHHIOIASTAKVTRTRGPGSCSNYDNLDSVSVLVQSPENKIQL 240
 DB 181 AASYFIDRSTLRLLHHIOIASTAKVTRTRGPGSCSNYDNLDSVSVLVQSPENKIQL 240
 QY 241 QGLQVLLPDYLOERFVQAALSYIACNSEGEFICKENDCWCPCGKPEPCNCPMDIOAME 300
 DB 241 QGLQVLLPDYLOERFVQAALSYIACNSEGEFICKENDCWCPCGKPEPCNCPMDIOAME 300
 QY 301 ENLLRITETWKAYNSDFEESDEFKFMKELPNYFLNTSTIMHLWTMDSNFQRRYEQLEN 360
 DB 301 ENLLRITETWKAYNSDFEESDEFKFMKELPNYFLNTSTIMHLWTMDSNFQRRYEQLEN 360
 QY 361 SMKQLFLKAQKIVHKLFSLSKCKHQPLISLPRQRTSTTWLTRIQSFLYCNENGLLGSPS 420
 DB 361 SMKQLFLKAHRIVHKLFSLSKCKHQPLISLPRQRTSTTWLTRIQSFLYCNENGLLGSPS 420
 QY 421 EETHSCTCPNDQVCTAFLECTVGDASACLTCPAPDNTRCGTCTGNTGYMLSGGLCKEVAE 480
 DB 421 EETHSCTCPNDQVCTAFLECTVGDASACLTCPAPDNTRCGTCTGNTGYMLSGGLCKEVAE 480
 QY 481 STDHYIGFETDLODLEKYLLOKTDRIEVAHFISNDMLNSWFDPSWKRMLLTLSN 540
 DB 481 STDHYIGFETDLODLEKYLLOKTDRIEVAHFISNDMLNSWFDPSWKRMLLTLSN 540
 QY 541 KYKSSLVHMLTGLSLQCLTKNSTLEPLVAVYVNPFGGSHSFWMPVNSPPDWERTK 600
 DB 541 KYKSSLVHMLTGLSLQCLTKNSTLEPLVAVYVNPFGGSHSFWMPVNSPPDWERTK 600
 QY 601 LDLPLOCYNWTILGNKWKTFETVHIYLSRSKNSGPNESIIYEPLEFIDPSRLGY 660
 DB 601 LDLPLOCYNWTILGNKWKTFETVHIYLSRSKNSGPNESIIYEPLEFIDPSRLGY 660
 QY 661 MKINNIQVFGYSMHFDPEARDLILQDYPYTOGSQDSALLQLLEIRDRVNLKSPPGQRR 720
 DB 661 MKINNIQVFGYSMHFDPEARDLILQDYPYTOGSQDSALLQLLEIRDRVNLKSPPGQRR 720
 QY 721 LDLPSCLLHRLKLTSEVVRISQALQAFNAKLPTMTDYDTTKLCS 766
 DB 721 LDLPSCLLHRLKLTSEVVRISQALQAFNAKLPTMTDYDTTKLCS 766

RESULT 3
 Q8KIM7 PRELIMINARY; PRT; 766 AA.
 ID Q8KIM7
 AC Q8KIM7
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE BNP/Retinoic acid-inducible neural-specific protein-3.
 GN Name=BRINP3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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NCBI_TaxID=10116;
SEQUENCE FROM N.A.
Matsuoaka I., Toda F., Nakatani T., Mori T., Ueno S., Kawano H.,
Kobayashi M.;
Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AB077854; BAC03100.1; -
InterPro; IPR006210; IEFG.
DR pfam; PF01823; MACPF, 1.
DR SMART; SM00181; EGF, 1.
DR SMART; SM00457; MACPF, 1.
SQ SEQUENCE 766 AA; 88496 MW; 0D210F602E1BE5D CRC64;

Query Match      98.0%; Score 3998; DB 2; Length 766;
Best Local Similarity 97.7%; Pred. No. 2.1e-279;
Matches 748; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 MIWRRAGAEFLSMALMEWIALSLHCWVLA VAAVSDQHATSPFDWLLSDKGPFFHRSQY 60
DB 1 MIWRRAGAEFLSMALMEWIVLSLHCWVLA VAAVSDQHATSPFDWLLSDKGPFFHRSQY 60

QY 61 TDFVDRSQGFSTRYKIYREFGRWKVNNAVRRNPLGSPPLAPEFFRNILLGRPTL 120
DB 61 TDFVDRSQGFSTRYKIYREFGRWKVNNAVRRNPLGSPPLAPEFFRNILLGRPTL 120

QY 121 QOITENLIKYGTHFLSATLGGEESLTFVDKRLSKRAEGSDTTNSSSVTLTTLHL 180
DB 121 QOITENLIKYGTHFLSATLGGEESLTFVDKRLSKRAEGSDTTNSSSVTLTTLHL 180

QY 181 AASYFIDRDLRLRHIIQIASTAIKVTETRTGPGCSNYDNLDSVSVLVQSPENKIQ 240
DB 181 AASYFIDRDLRLRHIIQIASTAIKVTETRTGPGCSNYDNLDSVSVLVQSPENKIQ 240

QY 241 QGLQVLLPDYLOERFVQAALSYIACNSGEFTCKENDCWCCKGPKFPCNCPSMDIQ 300
DB 241 QGLQVLLPDYLOERFVQAALSYIACNSGEFTCKENDCWCCKGPKFPCNCPSMDIQ 300

QY 301 ENLRITETWKAYNSDFESDEFKLFMKRLPMNYELNTSTIMHLWTMDSNFQRYEQLEN 360
DB 301 ENLRITETWKAYNSDFESDEFKLFMKRLPMNYELNTSTIMHLWTMDSNFQRYEQLEN 360

QY 361 SMKQLFLKAHRIVHKLFSLSKRCHQPLISLPQRTSTYTWLTRIQLSFLYCNENGLLSGFS 420
DB 361 SMKQLFLKAHRIVHKLFSLSKRCHQPLISLPQRTSTYTWLTRIQLSFLYCNENGLLSGFS 420

QY 421 EETHSCTCPNDQVCTAFPLCTVGDASACLTCPADNRTRCGTCNTGYMLSGCLCKPEVAE 480
DB 421 EETHSCTCPNDQVCTAFPLCTVGDASACLTCPADNRTRCGTCNTGYMLSGCLCKPEVAE 480

QY 481 STDHYIGETDLOLEMKYILQKTDRIEVAHAFISNDMRLNSWFPDPSWRKRMLLTLKSN 540
DB 481 STDHYIGETDLOLEMKYILQKTDRIEVAHAFISNDMRLNSWFPDPSWRKRMLLTLKSN 540

QY 541 KYKSLVHMLGLSLQICLTKNSTLEPVLAVVNPFGGSHSESMFNPVNSFPDWERTK 600
DB 541 KYKSLVHMLGLSLQICLTKNSTLEPVLAVVNPFGGSHSESMFNPVNSFPDWERTK 600

QY 601 LDPLQCYNTWTLTLGNKWKTFETFEVHYLRSRKISNGNPNESYIEPFEIDPSRNLYG 660
DB 601 LDPLQCYNTWTLTLGNKWKTFETFEVHYLRSRKISNGNPNESYIEPFEIDPSRNLYG 660

QY 661 MKINNIQVFGSMHFPDPAIRDILQLDYPYTOGSQDSALLQLLEIRDRVNKLSPPGQRR 720
DB 661 MKINNIQVFGSMHFPDPAIRDILQLDYPYTOGSQDSALLQLLEIRDRVNKLSPPGQRR 720

QY 721 LDLFCLLRHLRLKLSVSVVRIQSAQAFNAKLPNTMDYDTTKLCS 766
DB 721 LDLFCLLRHLRLKLSVSVVRIQSAQAFNAKLPNTMDYDTTKLCS 766
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RESULT 4
Q6DFY8

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ID AC DT 25-OCT-2004 (TRENBLrel. 28, Created)
RN Q6DFY8;
RP SEQUENCE FROM N.A.
RA Matsuoaka I., Toda F., Nakatani T., Mori T., Ueno S., Kawano H.,
RA Kobayashi M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DE EMBL; AB077854; BAC03100.1; -
DE BMP/retinoic acid-inducible neural-specific protein 2.
GN Name=6430517E21Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DE EMBL; BC076572; AAH76572.1; -
DR InterPro; IPR009030; Grow fac recept.
DR InterPro; IPR001862; MAC_perforin.
DR pfam; PF01823; MACPF, 1.
DR SMART; SM00457; MACPF, 1.
SQ SEQUENCE 783 AA; 89227 MW; CD78821BF51A5B6E CRC64;

Query Match      72.7%; Score 2968; DB 2; Length 783;
Best Local Similarity 70.9%; Pred. No. 4e-205;
Matches 547; Conservative 97; Mismatches 106; Indels 22; Gaps 5;

QY 17 LW-----EW---IALSLHCWVLA VAAVSDQHATSPFDWLLSDKGPFFHRSQY 60
DB 17 LW-----EW---IALSLHCWVLA VAAVSDQHATSPFDWLLSDKGPFFHRSQY 60

QY 121 QOITENLIKYGTHFLSATLGGEESLTFVDKRLSKRAEGSDTTNSSSVTLTTLHL 174
DB 121 QOITENLIKYGTHFLSATLGGEESLTFVDKRLSKRAEGSDTTNSSSVTLTTLHL 174

QY 175 ETLHQAASYFIDRDLRLRHIIQIASTAIKVTETRTGPGCSNYDNLDSVSVLVQSP 234
DB 175 ETLHQAASYFIDRDLRLRHIIQIASTAIKVTETRTGPGCSNYDNLDSVSVLVQSP 234

QY 192 ETLHQAASYFIDRDLRLRHIIQIASTAIKVTETRTGPGCSNYDNLDSVSVLVQSP 251
DB 192 ETLHQAASYFIDRDLRLRHIIQIASTAIKVTETRTGPGCSNYDNLDSVSVLVQSP 251

QY 235 ENKTOLOGVLLPDYLOERFVQAALSYIACNSGEFTCKENDCWCCKGPKFPCNCPSM 294
DB 235 ENKTOLOGVLLPDYLOERFVQAALSYIACNSGEFTCKENDCWCCKGPKFPCNCPSM 294

QY 252 ENKQVLLGLQVLLPEHLRERFVAAALSYITCSSEGLVCRENDWCCKSPFPBCNCDA 311
DB 252 ENKQVLLGLQVLLPEHLRERFVAAALSYITCSSEGLVCRENDWCCKSPFPBCNCDA 311

QY 295 DIOAMEENLRITETWKAYNSDFESDEFKLFMKRLPMNYELNTSTIMHLWTMDSNFQRR 354
DB 295 DIOAMEENLRITETWKAYNSDFESDEFKLFMKRLPMNYELNTSTIMHLWTMDSNFQRR 354
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Db 312 DIQAMEDSLQIQDSWATHNRQFESEEFQTLKRLPDRFLNSTAISQVWTMDSNLQHR 371
QY 355 YEOLSNMQLFLKAKQIVHKLFSLSKRCCHKOPLISLPRQRTSTYWLTRIQSFLYCNENG 414
Db 372 YOQLGASLVKLLKQKHRIVRRLFNLCRCHROPRFLPKERSLSFWNRIQSILLYCGEST 431
QY 415 LGSFSEETHSCTCPNDQVVTAFPLCTVGDASACLTACPDNRTRCGTCTNTGYMLSQGLC 474
Db 432 FPGTFLEQSHSCTCPYDQSSCOGPIPCALGEGPACAHACASDNSTRCGSNPGVYLAQGLC 491
QY 475 KPVEASTHYIGFTDLOLEMKYLLQKTDRIEIVHAFISNDMLNSWFDPSWKRML 534
Db 492 RPEVAESLENFLGLETDLQLELKYLLQKDRSRIEIVHSIFISNDMLGWSWFDPSWKRML 551
QY 535 LTLKSNKYKSSLVHMTLGLQICLTKNSTLEPVLAVYVNPFGGSHSESWFMPVNSFP 594
Db 552 LTLKSNKYKPLVHVNALSLQICLTKNSTLEPVMAYVNPFGGSHSESWFMPVNEGNFP 611
QY 595 DWERTKLDLPQCYNNWTLTLGNKWKTFEFTVHYILRSRIKSNPGNENESIYYEPLFIDP 654
Db 612 DWERTNVDAQAQCNWTLTLGNKWKTFEFTVHYILRSRIKSLDSSNETIYYEPLWMDP 671
QY 655 SRNLGYMKINNIQVFGSMHFDPEAIRDLILQDYPYTGQSODSALLQLEIRDRVNKL 714
Db 672 SKNLGYMKINTLQVFGYSLPDPDAIRDLILQDYPYTGQSODSALLQLEIRDRVNQLS 731
QY 715 PPGQRLDLFSCLLRHRLKLSSTSEVVRIQSALQAFNAKLNTMDYDTTKLCS 766
Db 732 PPGKVRDLDFSCLLRHRLKLANNEVGRIQSSURAFNSKLNPVEYETGKLCS 783

RESULT 5
O80T96 PRELIMINARY; PRT; 788 AA.
ID Q80T96
AC Q80T96
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MKIAA1747 protein (Fragment).
GN Names=6430517E2Rik; Synonyms=mkIAA1747;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:35-48 (2003).
DR EMBL; AK122549; BAC65831.1; -
DR MGD; MGI:2443333; 6430517E2Rik.
DR InterPro; IPR006210; IEFG.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
DR NON_TER 1
FT SEQUENCE 788 AA; 89748 MW; DF4189DAFD43705B CRC64;

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Query Match 72.6%; Score 2963; DB 2; Length 788;
Best Local Similarity 70.7%; Pred. No. 9.2e-205;
Matches 546; Conservative 97; Mismatches 107; Indels 22; Gaps 5;
QY 17 LW-----EW-----TALSHCWVLAVAA-----VSDQHATS-----PFDWLLSDKGFPHRSQRY 60
DB 17 LWPEAPAPVALLALGVPGWVLAVSATVAAPVPEQVSSAGQAPLDWLLTRDGFPHRAQRY 76

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QY 61 TDFVDRSGFSTRYKIVREFGRWKNVNLAVERRNPLSPGLPAPEFFRNIRLLGRRPTL 120
Db 77 ADFMERYQGFTRIRYIREFARWKNVNLALERRDFSLPLPAPEFFVNRIRLLGRRPNL 136
QY 121 QOITENLIKKGTHFLSATLGGEESLTFVDRKRLSKRAEGSDSTT-----NSSSVTL 174
Db 137 QOVTENLIKKGTHFLSATLGGEESLTFVDRKRLSKRSETTGPIPVVGGPGNSAVSL 196
QY 175 ETLHOLAASYFDRDSTLRRLLHHIOIASTAIKVTETRTGPGCSNDYDNLDSVSSVLVQSP 234
Db 197 ETLHOLAASYFDRDSTLRRLLHHIOIASTAIKVTETRTGPGCSNDYDNLDSVSSVLVQSP 256
QY 235 ENKIOLQGLVLLPYLQERFVQAALSYIACNSEGEFICKENDCWCCHGKPFECNCPSM 294
Db 257 ENKVOLLGLVLLPEHLRERFVAALSYITCSSEGLVCRENDCKCKCSPTPECCNCPDA 316
QY 295 DTQAMENLLRITETWKAYNSDPESDSFKLPMKRLPMNYFLNTSTIMHLWTMDSNFQRR 354
Db 317 DTQAMEDSLQIQDSWATHNRQFESEEFQTLKRLPDRFLNSTAISQVWTMDSNLQHR 376
QY 355 YEOLSNMQLFLKAKQIVHKLFSLSKRCCHKOPLISLPRQRTSTYWLTRIQSFLYCNENG 414
Db 377 YOQLGASLVKLLKQKHRIVRRLFNLCRCHROPRFLPKERSLSFWNRIQSILLYCGEST 436
QY 415 LGSFSEETHSCTCPNDQVVTAFPLCTVGDASACLTACPDNRTRCGTCTNTGYMLSQGLC 474
Db 437 FPGTFLEQSHSCTCPYDQSSCOGPIPCALGEGPACAHACASDNSTRCGSNPGVYLAQGLC 496
QY 475 KPVEASTHYIGFTDLOLEMKYLLQKTDRIEIVHAFISNDMLNSWFDPSWKRML 534
Db 497 RPEVAESLENFLGLETDLQLELKYLLQKDRSRIEIVHSIFISNDMLGWSWFDPSWKRML 556
QY 535 LTLKSNKYKSSLVHMTLGLQICLTKNSTLEPVLAVYVNPFGGSHSESWFMPVNSFP 594
Db 557 LTLKSNKYKPLVHVNALSLQICLTKNSTLEPVMAYVNPFGGSHSESWFMPVNEGNFP 616
QY 595 DWERTKLDLPQCYNNWTLTLGNKWKTFEFTVHYILRSRIKSNPGNENESIYYEPLFIDP 654
Db 617 DWERTNVDAQAQCNWTLTLGNKWKTFEFTVHYILRSRIKSLDSSNETIYYEPLWMDP 676
QY 655 SRNLGYMKINNIQVFGSMHFDPEAIRDLILQDYPYTGQSODSALLQLEIRDRVNKL 714
Db 677 SKNLGYMKINTLQVFGYSLPDPDAIRDLILQDYPYTGQSODSALLQLEIRDRVNQLS 736
QY 715 PPGQRLDLFSCLLRHRLKLSSTSEVVRIQSALQAFNAKLNTMDYDTTKLCS 766
Db 737 PPGKVRDLDFSCLLRHRLKLANNEVGRIQSSURAFNSKLNPVEYETGKLCS 788

RESULT 6
O95560 PRELIMINARY; PRT; 781 AA.
ID O95560
AC O95560
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhodes S.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035289; CAA22893.1; -
DR InterPro; IPR006210; IEFG.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
KW Hypothetical protein..
FT NON_TER 1

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SQ SEQUENCE 781 AA: 88116 MW: DFE3EB83A08B599 CRC64;
Query Match
Best Local Similarity 72.6%; Score 2962; DB 2; Length 781;
Matches 543; Conservative 99; Mismatches 109; Indels 18; Gaps 4;
QY 16 ALMEW---IALSLHCWLVAA-----VSDQHAT-----SPFDWLLSDKGPFFHRSQYETDF 63
DB 13 AVAPWTALLALGLPGWLVAVSATAAAVPEQHASVAGQHPDLMLLTDGRGPFHRAQYADF 72
QY 64 VDRSQGFSTRYKTYRIFRGKVNKNLAVERNFPGSLPLAPEFFRNIRLLGRPTLOOI 123
DB 73 MERYRQGFTRTYRIRYREFARWKNVNLALERKDFSLPLAPEFIRNIRLLGRPNLQOV 132
QY 124 TENLIKKGTHFLLSATLGGESLTI FVDKRLSKRAGSDSTT-----NSSSVTLETL 177
DB 133 TENLIKKGTHFLLSATLGGESLTI FVDKRLSKRAGSDSTT-----NSSSVTLETL 192
QY 178 HQLAASYFIDRSTLRLRHHIQAIASTAIKVETRTGPGCSNYDNLDSSVSVLVQSPENK 237
DB 193 HQLAASYFIDRSTLRLRHHIQAIASTAIKVETRTGPGCSNYDNLDSSVSVLVQSPENK 252
QY 238 IQQLQVLLPDYLOERFVQAALSYIACNSEGFEICKENDCWCCHCGKPFPCNCPSMDIQ 297
DB 253 VQLLGLQVLLPEYLRERFVAALSYITCSSEGEVCKENDCWCCKSPFPFPCNCPSMDIQ 312
QY 298 AMEENLRITETWKAYNSDFEESDEFKLFMKRLPMNYELNTSTIMHWTMDSNFORRYEQ 357
DB 313 AMEDSLQIQDSWATHNRQFEESEFQALLKRLPDDRLFNSTALISQFWAMDTSLQHYQQ 372
QY 358 LENSMMQQLFLKAQKIVHKLFSLSKRCRKHQPLISLPRORTSTYWLTRIQSFLYCNENGLLG 417
DB 373 LGAGLKVFLKTHRLRLRFLNLCRCHQPRFLPKERSLSYWNRIQSLLYCGESTFPG 432
QY 418 SFSSETHSCTCPNDQVCTAFPLCTVGDASACLTACAPDNTRCGTCTNGYMLSOGLCKRPE 477
DB 433 TFLQSHSCTCPYDQSSCQGPICPCALGEGPACAHCAPDNSTRCGSCNPGYVLAQGLCRPE 492
QY 478 VAESTDHYIGPETDLDLEMYKLLQKTRLEVHAIFISNDMLNSWEDPSWKRMLLTL 537
DB 493 VAESLENPLGLTDLQDLLEKYLQKQDSRLVHSIFISNDMLRGSWPDPSWKRMLLTL 552
QY 538 KSNKYKSLVHMLGLSLQICLTKNSTLEPVLAVVNPFGGSHSESWPMVNPENSFDPWE 597
DB 553 KSNKYKGLVHMLGLSLQICLTKNSTLEPVLAVVNPFGGSHSESWPMVNPENSFDPWE 612
QY 598 RTKLDLPLQCVNWTITLGNKWKTFETVHLYRLSRKISGNPNESIIYEPLEFIDPSRN 657
DB 613 RTNVDAQAQCNWTITLGNRWKTFETVHLYRLSRKISGLDSSNETIYEPLEMTDPSKN 672
QY 658 LGYMKINNIQVGYSMHFDPEAIRDLILQLDYPTQGSQDSALLQLEIRVNKLSPPG 717
DB 673 LGYMKINTQVGYSLPDPDAIRDLILQLDYPTQGSQDSALLQLEIRVNKLSPPG 732
QY 718 QRRDLFSLRLRHLKSLTSBWRVQISALQAFNAKLPMNTMDYDTTKLCS 766
DB 733 KYRLDLFSLRLRHLKLANNEVGRVQISLRAFNSKLPMNPVEYETGKLC 781

RESULT 7
Q8N360 PRELIMINARY; PRT; 783 AA.
AC Q8N360;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE BNP/retinoic acid-inducible neural-specific protein 2 (DBCCR1-
DE like2).
GN Name=KIAA1747; Synonyms=DBCCR1L2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;

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RN RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN RP SEQUENCE FROM N.A.
RA Inazawa J., Imoto I.;
RT "Homo sapiens DBCCR1L2 mRNA for DBCCR1-like2.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028036; AAH28036.1; -
DR EMBL; AB161694; BAD34946.1; -
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
SQ SEQUENCE 783 AA; 89004 MW; B8362095ADC97FCD CRC64;
Query Match
Best Local Similarity 72.6%; Score 2962; DB 2; Length 783;
Matches 543; Conservative 99; Mismatches 109; Indels 18; Gaps 4;
QY 16 ALMEW---IALSLHCWLVAA-----VSDQHAT-----SPFDWLLSDKGPFFHRSQYETDF 63
DB 15 AVAPWTALLALGLPGWLVAVSATAAAVPEQHASVAGQHPDLMLLTDGRGPFHRAQYADF 74
QY 64 VDRSQGFSTRYKTYRIFRGKVNKNLAVERNFPGSLPLAPEFFRNIRLLGRPTLOOI 123
DB 75 MERYRQGFTRTYRIRYREFARWKNVNLALERKDFSLPLAPEFIRNIRLLGRPNLQOV 134
QY 124 TENLIKKGTHFLLSATLGGESLTI FVDKRLSKRAGSDSTT-----NSSSVTLETL 177
DB 135 TENLIKKGTHFLLSATLGGESLTI FVDKRLSKRAGSDSTT-----NSSSVTLETL 194
QY 178 HQLAASYFIDRSTLRLRHHIQAIASTAIKVETRTGPGCSNYDNLDSSVSVLVQSPENK 237
DB 195 HQLAASYFIDRSTLRLRHHIQAIASTAIKVETRTGPGCSNYDNLDSSVSVLVQSPENK 254
QY 238 IQQLQVLLPDYLOERFVQAALSYIACNSEGFEICKENDCWCCHCGKPFPCNCPSMDIQ 297
DB 255 VQLLGLQVLLPEYLRERFVAALSYITCSSEGEVCKENDCWCCKSPFPFPCNCPSMDIQ 314
QY 298 AMEENLRITETWKAYNSDFEESDEFKLFMKRLPMNYELNTSTIMHWTMDSNFORRYEQ 357
DB 315 AMEDSLQIQDSWATHNRQFEESEFQALLKRLPDDRLFNSTALISQFWAMDTSLQHYQQ 374
QY 358 LENSMMQQLFLKAQKIVHKLFSLSKRCRKHQPLISLPRORTSTYWLTRIQSFLYCNENGLLG 417

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Db      375 LGAGLVKFKKTHRLRNLKRCRCHRPRLPKERSLSYWNRIQSLLYCGESTFPG 434
QY      418 SFSEETHSCPCNDQVCTAFLEPCTVGDASACLTCAPDNRTRCGTGTGNTGMLSQGLCKPE 477
Db      435 TFEQSHSCPCPYDQSCOCPIPCALGEGPACAHCAPDNRTRCGSCNPGVYLAQGLCRPE 494
QY      478 VAESTDIHYIGFETDLOLEMKYLLQKTDRIEIVHAFISNDMLNSWFDPSWKRMLLTL 537
Db      495 VAESLENFLGLETDLOLEKYLLOKDSRIEIVHSIFISNDMLNSWFDPSWKRMLLTL 554
QY      538 KSNKYKSSLVHMLIGLSLOICLTKNSTLEPVLAVYVNPFGGSHSSEWFMVNVNSFPDWE 597
Db      555 KSNKYKPGLVHVMALSLQICLTKNSTLEPVMAYVNPFGGSHSSEWFMVNEGSFPDWE 614
QY      598 RTKLDLPLOCYNWTLTLGNKWKTFEETVHLYLSRIKSNCPNGNESIYIEPLEFIDPSRN 657
Db      615 RTNVDAQAQCONWTTITLGNKWKTFEETVHLYLSRIKSLDSSNETIYIEPLEMTDPSKN 674
QY      658 LGYMKINNIQVFGYSMHFDPDAIRDILQLDYPTQGSQDSALLQLLEIRDRVKNLSPPG 717
Db      675 LGYMKINTLQVFGYSPFPDPAIRDILQLDYPTQGSQDSALLQLLEIRDRVKNLSPPG 734
QY      718 QRLDLFSCLLRHRLKLSSTSEVVRISALQAFNAKLPNTMDYDTTKLCS 766
Db      735 KVRLLDLFSCLLRHRLKLANNEVGRIQSSRAFNKLPNPVEYETGKLCS 783

RESULT 8
Q8KIM8 PRELIMINARY; PRT; 783 AA.
AC Q8KIM8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE EMP/Retinoic acid-inducible neurai-specific protein-2.
GN Name=BRINP2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsushita I., Ueno S., Nakatani T., Toda F., Mori T., Kawano H.,
RA Kobayashi M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB077853; BAC03099.1; -.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
SQ SEQUENCE 783 AA; 89138 MW; 2FF2F9532F62975D CRC64;

Query Match 72.6%; Score 2962; DB 2; Length 783;
Best Local Similarity 70.7%; Pred. No. 1.1e-204;
Matches 546; Conservative 97; Mismatches 107; Indels 22; Gaps 5;

QY 17 LW-----EW-----IALSLHCWLVAVAA-----VSDQHATS-----PFDWLLSDKGFPHRSQY 60
Db 12 LWPEAAPWAVLLALGPGWGLVAVSATVAAVVPQHVSSAGQAPLDWLLTDGRGPFHRAQY 71
QY 61 TDFVDSRQGSFTRYKIYREFGKWNVLAVERNFLGSLPLAPFERNIRLLGRPRTL 120
Db 72 ADMERYRQGFTRYRIYREFARKWNVLALERKDFSLPLPAPEFVNIRLLGRPNL 131
QY 121 QQITENLIKYGTHFLLSATLGGEESLTI FVDRKRLSKRAEG-----SDSTNSSSVTL 174
Db 132 QQVTENLIKYGTHFLLSATLGGEESLTI FVDRKRLSKRSETLGGVVPVGGTGNSSAVSL 191
QY 175 ETIHLQAASYFIDRDSITRLRLHHIQIASTAIVKTRTGTPLGCSNVDNLDSSVSLVQSP 234
Db 192 ETIHLQAASYFIDRDSITRLRLHHIQIATGAIVKTRTGTPLGCSNVDNLDSSVSLVQSP 251

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QY 235 ENKIQLQGLVLLPDYLOERFVQAALSYIACNSEGEFICKENDCWCCHGCKPKPFECNCPSM 294
Db 252 ENKVQLLQGLVLLPDYLOERFVQAALSYITCSEGLVLCRENDWCCKSPFTFPECNCPSM 311
QY 295 DIQAAMENLRITETWKAYNSDFEESDEFKJMKRLPMNYFLNTSTIMHLMTWDSNFQRR 354
Db 312 DIOAMEDSLQIODSWATHNRQFESEEPOTLLKRLPSDRFLNSTAISQVWTMDANLQHR 371
QY 355 YQLENSMKQLFLKAKIVHKLPSLSKCHKOPLSLPRQRTSTYWLTIQSLYLCNENG 414
Db 372 YOOLGASLVKLLKXHVIRVRLFNLCRCHRPRLPKERSLSFWMNRIOQLLYCGEST 431
QY 415 LLGFSSEETHSCPCNDQVCTAFLEPCTVGDASACLTCAPDNRTRCGTGTGNTGMLSQGLC 474
Db 432 PFGTFLEQSHSCPCPYDQSCOCPIPCALGEGPACAHCAPDNRTRCGSCNPGVYLAQGLC 491
QY 475 KPEVAESTDIHYIGFETDLOLEMKYLLQKTDRIEIVHAFISNDMLNSWFDPSWKRML 534
Db 492 RPEVAESLENFLGLETDLOLEKYLLOKDSRIEIVHSIFISNDMLNSWFDPSWKRML 551
QY 535 LTLKSNKYKSSLVHMLIGLSLOICLTKNSTLEPVLAVYVNPFGGSHSSEWFMVNVNSFP 594
Db 552 LTLKSNKYKPGLVHVMALSLQICLTKNSTLEPVMAYVNPFGGSHSSEWFMVNEGSFP 611
QY 595 DWERTKLDLPLOCYNWTLTLGNKWKTFEETVHLYLSRIKSNCPNGNESIYIEPLEFIDP 654
Db 612 DWERTNVDAQAQCONWTTITLGNKWKTFEETVHLYLSRIKSLDSSNETIYIEPLEMTDP 671
QY 655 SRNLGYMKINNIQVFGYSMHFDPDAIRDILQLDYPTQGSQDSALLQLLEIRDRVKNLS 714
Db 672 SRNLGYMKINTLQVFGYSPFPDPAIRDILQLDYPTQGSQDSALLQLLEIRDRVKNLS 731
QY 715 PPGQRLDLFSCLLRHRLKLSSTSEVVRISALQAFNAKLPNTMDYDTTKLCS 766
Db 732 PPGQRLDLFSCLLRHRLKLANNEVGRIQSSRAFNKLPNPVEYETGKLCS 783

RESULT 9
Q9COB6 PRELIMINARY; PRT; 791 AA.
AC Q9COB6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIAA1747 protein (Fragment).
GN Name=KIAA1747;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082932; PubMed=11214970;
RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:347-355(2000).
DR EMBL; AB051534; BAB21838.1; -.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
SQ SEQUENCE 791 AA; 89887 MW; 21C5C035AAAFCA89 CRC64;

Query Match 72.6%; Score 2962; DB 2; Length 791;
Best Local Similarity 70.6%; Pred. No. 1.1e-204;
Matches 543; Conservative 99; Mismatches 109; Indels 18; Gaps 4;

QY 16 ALWEW---IALSLHCWLVAVAA-----VSDQHAT-----SPFDWLLSDKGFPHRSQYTFD 63

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DB 23 AVAPWTALLALGLPGWVLAVSATAAAVVPQHASVAGQHPDLWLLTDRGPFHRAQEVADF 82
QY 64 VDRSROGFSTRYKIYREFGRGWKNVNLAVERRFLGSLPLAEPFFNIRILGRPTLOQI 123
DB 83 MEYRQGFTRIRYIREFARWKNVNLALERKQFSLPLAEPFIRNIRLLGRPNLOQV 142
QY 124 TENLIKKYTHFLLSATLGGESLTIFFVDRKLSKRAEGSDSTT-----NSSSVTLETL 177
DB 143 TENLIKKYTHFLLSATLGGESLTIFFVDRKLSKRAEGSDSTT-----NSSSVTLETL 202
QY 178 HOLAAASYFDRDSTLRRLHHIQIASTAIKVTETRTGPGCSNYDNLDSSVSVLVQSPENK 237
DB 203 HOLAAASYFDRDSTLRRLHHIQIASTAIKVTETRTGPGCSNYDNLDSSVSVLVQSPENK 262
QY 238 IOLOGLQVLLPDLQYORFVQAALSYIACNSEGEFICKENDCHCQKPEPCNCPSMDIO 297
DB 263 VOLLLGLOVLLPYLRERFVAALSYITCSSEGLVCKENDCKCKSPPTPEPCNCPDADIQ 322
QY 298 AMEENLRITETWKAYNSDFEESDEFKLFMKRLPMNYFLTSTIMHLWTMDSNFORRYEQ 357
DB 323 AMEDSLQIODSWATHNRQFESEEFQALLKRLPDRFLNSTAIQFWMADTSLQHRYYQ 382
QY 358 LENSXKQPLKQAKIVHKLFSLSKCHQKPLISLPRQRTSTYMLTRIQSFLYCNENGLG 417
DB 383 LGAGLKVLPKTHIRILRFLNLCKRCHQRPRLPKERSLSYWMNRIOQLLYCGESTFPG 442
QY 418 SPSEETHSCPCNDQVCTAFPLCTVGDASACLTCAPONRTRCGTCNTGYMLSQGLCKPE 477
DB 443 TPLEQSHSCPCPYDSSQCGPIPCALGEGPACAHCAPDNSTRCGSCNPGYVLAQGLCKPE 502
QY 478 VAESDHYIGFTDQLEMKYLLQKTRRIEIVHAFISNDMLNSWDPSPWRKMLLT 537
DB 503 VAESLENFLGLETDLQLEKYLKQDSRIEIVHSIFISNDMLNSWDPSPWRKMLLT 562
QY 538 KSNKYKSSLVHMLGLSLQICLTKNSTLEPVLAVYVNPFGGSHSSEWMPVNEGSFPDWE 597
DB 563 KSNKYKPLGVHMLALSQICLTKNSTLEPVLAVYVNPFGGSHSSEWMPVNEGSFPDWE 622
QY 598 RTKLDLPQCYNWTITLGNKWKTFETVHIYLSRIKSNPGNPNESIIYEPLEFIDPSRN 657
DB 623 RTNVDAAQCCQNTITLGNRWKTFETVHVYLSRIKSLDDSSNETIYIEPLEMTDPSKN 682
QY 658 LGYKINNIQVGYSMHPDPAIRDLILQLDYPTQGSODSALLQLEIRDRVNLKSPG 717
DB 683 LGYKINNIQVGYSLPDPDAIRDLILQLDYPTQGSODSALLQLEIRDRVNLKSPG 742
QY 718 QRRDLFSCLLRHLKLTSTSEVVRIOQALQAFNAKLPTNMDYDTTKLCS 766
DB 743 KVRDLFSCLLRHLKLTSTSEVVRIOQALQAFNAKLPTNMDYDTTKLCS 791

RESULT 10
Q6ZWC1 ID Q6ZWC1 PRELIMINARY; PRT; 678 AA.
AC Q6ZWC1;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ41342.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBT_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
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RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AKI23336; BAC85583.1; -.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00457; MACPF; 1.
SQ SEQUENCE 678 AA; 76520 MW; F34E4C754AC2612C CRC64;

Query Match 60.6%; Score 2474.5; DB 2; Length 678;
Best Local Similarity 70.5%; Pred. No. 1.3e-169;
Matches 451; Conservative 86; Mismatches 96; Indels 7; Gaps 2;

QY 133 THFLLSATLGGESLTIFFVDRKLSKRAEGSDSTT-----NSSSVTLETLHQLAASYFI 186
DB 40 TNLVLFPI-GEESLTIFFVDRKLSKRAEGSDSTT-----NSSSVTLETLHQLAASYFI 98
QY 187 DRDSTLRRLHHIQIASTAIKVTETRTGPGCSNYDNLDSSVSVLVQSPENKIQLOGLQVL 246
DB 99 DRESTLRRLHHIQIASTAIKVTETRTGPGCSNYDNLDSSVSVLVQSPENKIQLOGLQVL 158
QY 247 LPDYLOERFVQAALSYIACNSEGEFICKENDCHCQKPEPCNCPSMDIOAMEENLR 306
DB 159 LPEYLRERFVAALSYITCSSEGLVCKENDCKCKSPPTPEPCNCPDADIQAMEDSLQI 218
QY 307 TETWKAYNSDFEESDEFKLFMKRLPMNYFLTSTIMHLWTMDSNFORRYEQLENSXKQPL 366
DB 219 QDSWATHNRQFESEEFQALLKRLPDRFLNSTAIQFWMADTSLQHRYYQGLKVL 278
QY 367 LKAOKIVHKLFSLSKCHQKPLISLPRQRTSTYMLTRIQSFLYCNENGLLSFSBETHSC 426
DB 279 KKTIRLLRLLNLCKRCHQRPRLPKERSLSYWMNRIOQLLYCGESTFPGTFLQSHSC 338
QY 427 TCPNDQVCTAFPLCTVGDASACLTCAPONRTRCGTCNTGYMLSQGLCKPEVAESDHYI 486
DB 339 TCPYDQSSQCGPIPCALGEGPACAHCAPDNSTRCGSCNPGYVLAQGLCKPEVAESLEN 398
QY 487 GFETDQLEMKYLLQKTRRIEIVHAFISNDMLNSWDPSPWRKMLLTLSKNYKSL 546
DB 399 GLETDQLEMKYLLQKTRRIEIVHAFISNDMLNSWDPSPWRKMLLTLSKNYKSL 458
QY 547 VHMILGLSLQICLTKNSTLEPVLAVYVNPFGGSHSSEWMPVNEGSFPDWEKTLDPQ 606
DB 459 VHMILGLSLQICLTKNSTLEPVLAVYVNPFGGSHSSEWMPVNEGSFPDWEKTLDPQ 518
QY 607 CYNWTLTGNKWKTFETVHIYLSRIKSNPGNPNESIIYEPLEFIDPSRLNGYKINNI 666
DB 519 CQNTITLGNRWKTFETVHVYLSRIKSLDDSSNETIYIEPLEMTDPSKNGYKINNI 578
QY 667 QVFCYSMHFDPDAIRDLILQLDYPTQGSODSALLQLEIRDRVNLKSPGQRRDLFSC 726
DB 579 QVFCYSMHFDPDAIRDLILQLDYPTQGSODSALLQLEIRDRVNLKSPGQRRDLFSC 638

727 LLRHLKLTSTSEVVRIOQALQAFNAKLPTNMDYDTTKLCS 766
639 LLRHLKLTSTSEVVRIOQALQAFNAKLPTNMDYDTTKLCS 678

RESULT 11
Q7ZZR3 ID Q7ZZR3 PRELIMINARY; PRT; 761 AA.
AC Q7ZZR3;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE BMP/retinoic acid-inducible neural-specific protein.
GN Name=BRINP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBT_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
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RC TISSUE=Brain;
RA Stubbusch J.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ558161; CAD90040.1; -.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0007049; P:cell cycle; ISS.
DR GO; GO:0008219; P:cell death; ISS.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00457; MACPF; 1.
DR SEQUENCE 761 AA; 88790 MW; 8D0803F5910D1473 CRC64;
SQ
Query Match 53.5%; Score 2184; DB 2; Length 761;
Best Local Similarity 52.8%; Pred. No. 1.3e-148;
Matches 410; Conservative 134; Mismatches 205; Indels 28; Gaps 10;
QY 1 MIWRSAGAEFLSMALWEMIALS-LHCWVLAVAASDOHATSPEDWLLSDKGPHRSOE 59
DB 1 MNWRL---VEFLYLLFIWDHILVQPSH---QDPAATNQHVSKEFDWLLSDRGPFHRS 53
QY 60 YTDVDRSQGFSTRYKIYREFGRWKVNNLAVERNFGLSPLPLAPEFRNIRLLGRPT 119
DB 54 YLSFVERHQGFTRYKIYREFARWKVNTAIEDLLHNPLPLMPEFORSIRLLGRPT 113
QY 120 LQQTENLIKKGTHFLLSATLGGESLTI FVDKRLSKRAGSDSTTSSSVTLTLHQ 179
DB 114 TQQFIDTIIKKYTHLLISATLGGEEALTYMDKSL-----DRKSGNATQSVLEALHQ 166
QY 180 LAASYFIDRDLRLRHIIQIASTAIKVTETRTGPGSCSYNDLSDVSVLVQSPENKIQ 239
DB 167 LASSYFVDRDGMRLRLHEIQISTGAIKVETRTGPGSCSYNDLSDVSVLVQSTESKUH 226
QY 240 LQGLQVLLPDYLOERFVQAALSYIACNSEGEFICKENDCWCHGKPFPCNCPMDIQAM 299
DB 227 LQGLQIIFPQYLOEKFVQSALSYIMCNGEYLCQNSQCQCAEEFPQCNCPTIDIQM 286
QY 300 EENLLRITETWKAYNSDPEESDEFKLFMKRLPMNYFLNTSTIMHLWTMDSNFQRYEOL 359
DB 287 EYTLANMAKTWEAYKYLENSDEFKSFMKRLPSNHLFTIASIHQWGNWDWLDQNRKLLQ 346
QY 360 NSMKQLFLKAQIVHKLFLSKRCHKQPLISLPRQRTSTYMLTRIQSFLYCNENGLLSGF 419
DB 347 SSLEAQROKIQIORTARKLFGLSVRCRHNPNHQLPRETIQEWLTRYQSLYCNENGFWGT 406
QY 420 SEETHSCTCPNDQVQVCTAFPLCTVGDASACLTAPDNRTRCTGTCNTGYMLSOGLCKPEVA 479
DB 407 LESQSCVCHGTSGLCQRPICPIIGGNSCAMCSLANISLCGSCNKGKYLGRCEPQNV 466
QY 480 ES--TDHYIGFETDL--ODLEMKYLLQKTDRIEVAHFISNDMLNSWFDPSWKRMLL 535
DB 467 DSRSEQIFSFETDLDFOLEKYLQKWDRLYVHTTIFISNEIRLDTFFDPRWKRMSL 526
QY 536 TLKSNKYKSSLVHMLGLSLOICLTNKTLEPVLAVYVNPFGGSHSESMFMPVNSPDP 595
DB 527 TLKSNKRMDFIHVIGISMRICQENSSLDPMFVYVNPFGSGHSEGMNMPFGEVGYPR 586
QY 596 WERTKLDLPLQCYNWTLTGKWKTFETVHIYLSRIKSNPGNENSIYYBPLEFIDPS 655
DB 587 WEKIRLQ-NSQCYNWTLLGNRKWTFETVHIYLSRTRPLRLPILLSNET-GOGFVLDSPS 644
QY 656 RNLYGMKINNIQVGYSMHFDPEARTDILQIDPYTQSGO---DSALLQLLETRDRVN 711
DB 645 KEQFYIKISDVQYIGSLRFDNLRLASVQVQNSQYTGQGYFSSSVMLLLDTRDRIN 704
QY 712 KLSF---PQORLDLFSCLLRHLKLSTSEVRIQSALQAFNAKLNTWTDYTTKLC 765
DB 705 RLAPPVAPCKPQLDLSCKLKHRLKLTNSEILRVNHALDYNTIELKQSDQMTAKLC 761
PRELIMINARY; PRT; 761 AA.
RESULT 12
O60477
ID O60477
AC O60477;

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Db 587 WEKIRLQ-NSQCYNTWLLGNRKWTFETVHLYRSKTRPLTLRNET-GQGPVLSLSDPS 644
Qy 656 RNLYGYNKINNIOVFGYSMEHDPFAIRDLILQLDYPTQSGQ-----DSALLQLELRDRVN 711
Db 645 KQFYIKISDVQVFGYSLRFNADLLRSVQVQVNSQYTOGGQFYSVSSVMLLLDIDRIN 704
Qy 712 KLSP---PGQRRDLFSCLLRHRLKLSSTSEVVRISQALQAFNAKLNTMDYDTTKLC 765
Db 705 RLAPPVAPGPKQLDLFSCMLKHLKLTNSEIIRVNHALDLYNTEILKQSDQMTAKLC 761

RESULT 13
Q6PIAO PRELIMINARY; PRT; 761 AA.
AC Q6PIAO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Deleted in bladder cancer 1.
GN Name=DBC1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schenker C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Grumet J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065196; AAHG5196.1;
DR InterPro; IPR001862; MACP_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00457; MACPF; 1.
SQ SEQUENCE 761 AA; 88760 MW; 16FF47082FD52252 CRC64;

Query Match 53.0%; Score 2161; DB 2; Length 761;
Best Local Similarity 52.3%; Pred. No. 5.9e-147;
Matches 406; Conservative 134; Mismatches 209; Indels 28; Gaps 10;

Qy 1 MIMSRAGAEFLSMALMEWIALS-LHCWLVAAVSDQHATSPFDWLLSDKGPFFHSQE 59
Db 1 MNWRF---VELLYELFTWIGRISVQPSH---QEPAGTDQHVSKFEDWLISDRGFFHSRS 53
Qy 60 YTDVFSRQGSFTRYKTYRFGWKVNNLAVERNFGLSPPLAPFFRNIRLLGRPT 119
Db 54 YLSFVERHQGFTRYKTYRFAWKVNTAIERDLVRHVPVLMPEFQSRILLGRPT 113
Qy 120 LQQTENLIKKGTHFLLSATLGGEESLTFVDRKRLSKRAEGSDSTTNSSSVLTLELHQ 179

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Db 114 TQQFDITTKKKGTHLLSATLGGEALTMWMDKRL-----DRKSGNATQSVLALHQ 166
Qy 180 LAASYFIDRDSTLRRLHHIQIASTAIKVTETRTGPGCSYNDNLDSDSVSVLVQSPENKIQ 239
Db 167 LASSYFVDRDGTMRRLHEIQISTGAIKVTETRTGPGCSYNDNLDSDSVSVLVQSTESKLH 226
Qy 240 LOGQLVLLPDYLOERFVQAALSYIACNSEGEFICKENDCWCCHGCKPFCPCNCPMDIQAM 299
Db 227 LOGLOIIFPOYLQERFVQSALSYIMCNGEYELQNSQCRCQCAEEFPQCNCPITDIQIM 286
Qy 300 EENLLRITITWKAYNSDFEESDEFKLFMKRLPMNYFLNTSTIMHLWTMDSNFORRYEQLE 359
Db 287 EYTLANMAKSWAEAYKDLSENDEFKLFMKRLPSNHLFTIGSHQHWGNDWDLQNRVLLQ 346
Qy 360 NSMKOLFKAQKIVHKLFSLSKRCCHKQPLISLPRORTSTYMLTRIQSFLYCNENGLGSF 419
Db 347 SATEAQROKIQRTARKLFGLSVRCRHNPNHQLPRETTIQOMLARYQSLLYCNENGFMTF 406
Qy 420 SEETHSCTCPNDVVCTAFPLCTVGDASACLTCPADNTRCGTCNTGYMLSGCLCKPEVA 479
Db 407 LESRSCVCHGSTTLCQRPICPVIGNNSCAMCSLANISLQSCNKGKLYRGRCEPQNV 466
Qy 480 ES--TDHYIGFETDL--ODLEWKYLLQKTDRIEVEHAFISNDMLNSWFDPSWRKRMEL 535
Db 467 DSESEQIFSETDLDPQDLKYLQKMDRLYVHTTFISNEIRLDTFFDRWRKRMEL 526
Qy 536 TLKNKYKSSLVHMLGLSLQICLTQNSTLPEVLAVYVYVPGGSHSESWFMFVNSFPD 595
Db 527 TLKSNKRNMDFIHNVIGMSRMCQWRNSSLDPMFPVYVYVPGGSHSESWFMFVNGFYPR 586
Qy 596 WERTKLDLPQCYNTWLLGNRKWTFETVHLYRSKTRPLTLRNET-GQGPVLSLSDPS 644
Db 587 WEKIRLQ-NSQCYNTWLLGNRKWTFETVHLYRSKTRPLTLRNET-GQGPVLSLSDPS 644
Qy 656 RNLYGYNKINNIOVFGYSMEHDPFAIRDLILQLDYPTQSGQ-----DSALLQLELRDRVN 711
Db 645 KQFYIKISDVQVFGYSLRFNADLLRSVQVQVNSQYTOGGQFYSVSSVMLLLDIDRIN 704
Qy 712 KLSP---PGQRRDLFSCLLRHRLKLSSTSEVVRISQALQAFNAKLNTMDYDTTKLC 765
Db 705 RLAPPVAPGPKQLDLFSCMLKHLKLTNSEIIRVNHALDLYNTEILKQSDQMTAKLC 761

RESULT 14
Q920P3 PRELIMINARY; PRT; 760 AA.
AC Q920P3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE BMP/retinoic acid-inducible neural-specific protein (BRINP) (Mus
DE musculus adult male corpora quadrigemina cDNA, RIKEN full-length
DE enriched library, clone:B230117A03 product:deleted in bladder cancer
DE chromosome region candidate 1 (human), full insert sequence) (Deleted
DE in bladder cancer chromosome region candidate 1).
GN Name=Dccer1; Synonyms=BRINP;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Matsuoka I., Nakatani T., Kawano H., Kobayashi M., Matsumoto K.,
RA Ariga H., Abe A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."

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Db 705 LAPPVAPGKQDLDFSCMLKRLKLTNSEIIRVNHADLYNTEILKQSDQMTAKLC 760

Search completed: October 17, 2005, 12:47:24
Job time : 180 secs